

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/S26,324
Source: PCT
Date Processed by STIC: 3-16-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/16/2005

PATENT APPLICATION: US/10/526,324

TIME: 08:21:12

Input Set : E:\401uspc.app.txt

Output Set: N:\CRF4\03162005\J526324.raw

5 <110> APPLICANT: Imanaka, Takayuki
 6 Atomi, Haruyuki
 9 <120> TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
 10 HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
 11 THE SAME
 14 <130> FILE REFERENCE: 490051.401USPC
 C--> 17 <140> **CURRENT APPLICATION NUMBER: US/10/526,324**
 18 <141> CURRENT FILING DATE: 2005-02-28
 20 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/003597
 21 <151> PRIOR FILING DATE: 2003-08-29
 23 <150> PRIOR APPLICATION NUMBER: JP 2002-319011
 24 <151> PRIOR FILING DATE: 2002-08-30
 26 <160> NUMBER OF SEQ ID NOS: 2167
 30 <170> SOFTWARE: PatentIn version 3.1
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 2089378
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Thermococcus kodakaraensis KOD1
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 44 <222> LOCATION: (1)..(5016)
 45 <223> OTHER INFORMATION: DNA polymerase elongation subunit (family B)
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 53 <222> LOCATION: (5134)..(5733)
 55 <223> OTHER INFORMATION: Predicted metal-dependent hydrolase
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 65 <223> OTHER INFORMATION: Predicted CoA-binding protein
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 73 <222> LOCATION: (16696)..(17697)
 75 <223> OTHER INFORMATION: ABC-type sulfate/molybdate transport systems
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 83 <222> LOCATION: (23947)..(24834)
 85 <223> OTHER INFORMATION: Zn-dependent hydrolases
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 93 <222> LOCATION: (27565)..(28620)
 95 <223> OTHER INFORMATION: ATPase involved in DNA repair
 99 <220> FEATURE:

(pg. 6-7)

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103 <222> LOCATION: (29782)..(30681)
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113 <222> LOCATION: (31102)..(31266)
115 <223> OTHER INFORMATION: Uncharacterized ArCR
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123 <222> LOCATION: (31414)..(32235)
125 <223> OTHER INFORMATION: SAM-dependent methyltransferases COG0500 SmtA
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135 <223> OTHER INFORMATION: Archaeal flagellins
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145 <223> OTHER INFORMATION: Putative archaeal flagellar protein G
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175 <223> OTHER INFORMATION: Serine/threonine protein kinases
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195 <223> OTHER INFORMATION: Nicotinamide mononucleotide adenylyltransferase
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213 <222> LOCATION: (62830)..(63723)
215 <223> OTHER INFORMATION: Integrase
219 <220> FEATURE:
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223 <222> LOCATION: (67399)..(68973)
 225 <223> OTHER INFORMATION: Subtilisin-like serine proteases
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 235 <223> OTHER INFORMATION:
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 245 <223> OTHER INFORMATION: Phytoene dehydrogenase and related proteins
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 265 <223> OTHER INFORMATION: Fe-S oxidoreductases
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 275 <223> OTHER INFORMATION: Serine proteases of the peptidase family S9A
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 316 <223> OTHER INFORMATION: Glycine/D-amino acid oxidases (deaminating)
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 326 <223> OTHER INFORMATION: Uncharacterized ACR
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 334 <222> LOCATION: (106210)..(106779)
 336 <223> OTHER INFORMATION: Transcription initiation factor TFIID (TATA-binding protein)
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 384 <222> LOCATION: (188074)..(189315)
 386 <223> OTHER INFORMATION: Nucleoside-diphosphate-sugar pyrophosphorylases involved in
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 387 olysaccharide biosynthesis/translation initiation factor eIF2B su
 388 bunits COG1208 GCD1
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 408 <223> OTHER INFORMATION: Fimbrial assembly protein
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 436 <222> LOCATION: (204472)..(205083)
 438 <223> OTHER INFORMATION: ATP phosphoribosyltransferase (histidine biosynthesis)
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 446 <222> LOCATION: (209476)..(210486)
 448 <223> OTHER INFORMATION: Histidinol-phosphate aminotransferase/Tyrosine
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 456 <222> LOCATION: (212938)..(214239)
 458 <223> OTHER INFORMATION: Anthranilate/para-aminobenzoate synthases component I
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 459 E

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469 <223> OTHER INFORMATION: Phosphoribosylanthranilate isomerase
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477 <222> LOCATION: (244591)..(245055)
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517 <222> LOCATION: (276688)..(277758)
519 <223> OTHER INFORMATION: Aldehyde:ferredoxin oxidoreductase
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527 <222> LOCATION: (277759)..(278526)
529 <223> OTHER INFORMATION: ABC-type thiamine transport system
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537 <222> LOCATION: (281104)..(282072)
539 <223> OTHER INFORMATION: Putative periplasmic protein kinase ArgK and related GTPases
of G
540      3E family
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550 <223> OTHER INFORMATION: Predicted nucleic acid-binding protein
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558 <222> LOCATION: (294346)..(294663)
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580 <223> OTHER INFORMATION: Glycosyltransferases involved in cell wall biogenesis

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Input Set : E:\401uspc.app.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 414542
Seq#:1; N Pos. 786890,786907,786944,786945,786946
Seq#:1; N Pos. 839139
Seq#:1; N Pos. 1128488,1128499,1128505,1128506,1128517,1128518,1128539
Seq#:1; N Pos. 1128540
Seq#:1; N Pos. 1561400,1561477,1561545
Seq#:1; N Pos. 1767941
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Seq#:342; N Pos. 839139
Seq#:342; N Pos. 1128488,1128499,1128505,1128506,1128517,1128518,1128539
Seq#:342; N Pos. 1128540
Seq#:342; N Pos. 1561400,1561477,1561545
Seq#:342; N Pos. 1767941
Seq#:723; N Pos. 414542
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Seq#:723; N Pos. 1128540
Seq#:723; N Pos. 1561400,1561477,1561545
Seq#:723; N Pos. 1767941
Seq#:1087; N Pos. 321437
Seq#:1087; Xaa Pos. 21477
Seq#:1087; N Pos. 527833,527901,527978
Seq#:1087; N Pos. 960838,960839,960860,960861,960872,960873,960879,960890
Seq#:1087; Xaa Pos. 47772,47775
Seq#:1087; N Pos. 1250239
Seq#:1087; N Pos. 1302432,1302433,1302434,1302471,1302488
Seq#:1087; N Pos. 1674836
Seq#:1164; Xaa Pos. 110
Seq#:1266; Xaa Pos. 145
Seq#:1267; Xaa Pos. 3
Seq#:1469; N Pos. 321437
Seq#:1469; N Pos. 527833,527901,527978
Seq#:1469; Xaa Pos. 26066,26089,26115
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Seq#:1469; N Pos. 960860,960861,960872,960873,960879,960890
Seq#:1469; N Pos. 1250239
Seq#:1469; N Pos. 1302432,1302433,1302434,1302471,1302488
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Seq#:1469; N Pos. 1674836
Seq#:1563; Xaa Pos. 351,374,400
Seq#:1718; Xaa Pos. 114,115
Seq#:1838; N Pos. 321437

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Seq#:1838; N Pos. 527833,527901,527978
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Seq#:1838; Xaa Pos. 49118
Seq#:1838; N Pos. 1302432,1302433,1302434,1302471,1302488
Seq#:1838; N Pos. 1674836
Seq#:2033; Xaa Pos. 167

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Output Set: N:\CRF4\03162005\J526324.raw

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L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:235
L:370 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:356
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L:2332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:2318
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L:3542 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:3528
L:3562 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:3548
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M:341 Repeated in SeqNo=342
L:343009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:723 after pos.:414485
M:341 Repeated in SeqNo=723
L:500845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1087 after pos.:321405
M:341 Repeated in SeqNo=1087
L:588226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1164 after pos.:96
L:607643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1266 after pos.:144
L:607779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1267 after pos.:0
L:662821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1469 after pos.:321429
M:341 Repeated in SeqNo=1469
L:754490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1563 after pos.:336
M:341 Repeated in SeqNo=1563
L:783883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1718 after pos.:112
L:822617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1838 after pos.:321377
M:341 Repeated in SeqNo=1838
L:931120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2033 after pos.:160